

110677

Schreiber, David

From: Ramirez, Delia
Sent: Monday, December 15, 2003 6:47 PM
To: Schreiber, David
Subject: case 09/866379

Hi,

I would like to request the following alignments:

1. seq id 5, 6, 7 against seq id 9 (nucleic acids)
2. seq id 8 against seq id 10 (proteins)
3. seq id 8 against seq id 7
4. seq id 10 against seq id 9

Thank you,

De's M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
1911 S. Clark Street, Crystal Mall 1, 10D06, Mail room 10D01
Arlington, VA 22202
(703) 306-0288
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```
QY 841 CGCAGCCAGAGGTTGCGCGCAGCGCGCCACCCCGTTATTAGATTGATCAGACAGCG 900
DB 1028 CGCAGCCAGAGGTTGCGCGCAGCGCGCCACCCCGTTATTAGATTGATCAGACAGCG 1087
QY 901 TTGAGCGCCCAATCCACCGCAGGAGGATGATGATGATGATGATGATGATGATGATG 960
DB 1088 TTGAGCGCCCAATCCACCGCAGGAGGATGATGATGATGATGATGATGATGATGATG 1147
QY 961 TTTATCGCGGACAGATTAATCTGCGCAATCTGCGCGGCGGCGGCGGCGGCGGCGGCG 1020
DB 1148 TTTATCGCGGACAGATTAATCTGCGCAATCTGCGCGGCGGCGGCGGCGGCGGCGGCG 1207
QY 1021 AGCTTCCCGGTCAGCGGAGTAACCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
DB 1208 AGCTTCCCGGTCAGCGGAGTAACCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1267
QY 1081 CTTGCGCTAAGGATTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
DB 1268 CTTGCGCTAAGGATTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1327
QY 1141 CAGATCGGTAAGGATTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
DB 1328 CAGATCGGTAAGGATTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1387
QY 1201 CTTGCGGAGGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
DB 1388 CTTGCGGAGGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1447
QY 1261 ATCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1300
DB 1448 ATCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1487
```

RESULT 2

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US-09-866-379C-5
; Sequence 5, Application US/09866379C
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Barton, Nelson Robert
; APPLICANT: Garret, James B.
; APPLICANT: O' Donoghue, Eileen
; APPLICANT: Mathur, Eric J.
; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 09010-029006
; CURRENT APPLICATION NUMBER: US/09/866,379C
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/580,515
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 09/318,528
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 09/291,931
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: US 09/259,214
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/910,798
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1901
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 403
; OTHER INFORMATION: n = A,T,C or G
US-09-866-379C-5
```

Query Match 96.9%; Score 1267; DB 1; Length 1901;
Best Local Similarity 98.4%; Pred. No. 0;

```
Matches 1279; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 ATGAAGCGGATCTTAATCCCATTTTATCTCTTCATGATTCGTTAAACCGCGCAATCTGCA 60
DB 188 ATGAAGCGGATCTTAATCCCATTTTATCTCTTCATGATTCGTTAAACCGCGCAATCTGCA 247
QY 61 TTGCGTCAGAGTGAGCGGAGCTGAAGCTGGAAGTGTGTGTGATTTCTAGTCTCATGTT 120
DB 248 TTGCGTCAGAGTGAGCGGAGCTGAAGCTGGAAGTGTGTGTGATTTCTAGTCTCATGTT 307
QY 121 GTGCGTCTCAACCAAGGCGACGCACTGATGATGATGATGATGATGATGATGATGATG 180
DB 308 GTGCGTCTCAACCAAGGCGACGCACTGATGATGATGATGATGATGATGATGATGATG 367
QY 181 ACTTGGCGGCTTAAACTTGGGTGAGCTGACACCGCGGCTGCTGATTAATTCGCTATCTC 240
DB 368 ACTTGGCGGCTTAAACTTGGGTGAGCTGACACCGCGGCTGCTGATTAATTCGCTATCTC 427
QY 241 GGCATTTACTTGGCGTCTGAGCTCTGAGTACGAGGATGCTGCTTAATTTGCTGCTGCG 300
DB 428 GGCATTTACTTGGCGTCTGAGCTCTGAGTACGAGGATGCTGCTTAATTTGCTGCTGCG 487
QY 301 CAGTCTGCTCAGCTTCCGATTTTCTGATGATGATGATGATGATGATGATGATGATG 360
DB 488 CAGTCTGCTCAGCTTCCGATTTTCTGATGATGATGATGATGATGATGATGATGATG 547
QY 361 GCCTTCCGCGCGGCTGCGACCTGACTGTGCAATAACCGTACATATCCAGGCGAGATACG 420
DB 548 GCCTTCCGCGCGGCTGCGACCTGACTGTGCAATAACCGTACATATCCAGGCGAGATACG 607
QY 421 TCCAGTCCCGATCCGTTTAAATTCCTCTATAAACTGCGCTTTGCGCAATCAAACTTGTGC 480
DB 608 TCCAGTCCCGATCCGTTTAAATTCCTCTATAAACTGCGCTTTGCGCAATCAAACTTGTGC 667
QY 481 AACGTGATGACCGATCTCTCGAGCGGCGAGGAGGCTCAATTCGCTGCTTTACCGGCGAT 540
DB 668 AACGTGATGACCGATCTCTCGAGCGGCGAGGAGGCTCAATTCGCTGCTTTACCGGCGAT 727
QY 541 TATCAAAACCGGCTTTCGCAACTCGAACTGCGCTGCTTAATTTTCGCAATCAAACTTGTGC 600
DB 728 CCGCAAAACCGGCTTTCGCAACTCGAACTGCGCTGCTTAATTTTCGCAATCAAACTTGTGC 787
QY 601 CTTAAACGTGAGAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 788 CTTAAACGTGAGAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 847
QY 661 AAGGTGAGCGCGACTGTGCTCTCAATTAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 848 AAGGTGAGCGCGACTGTGCTCTCAATTAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907
QY 721 GAGATATTTCTCTCTGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 908 GAGATATTTCTCTCTGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 967
QY 781 GATTCACACGAGTGAACACCTTCTGATGATGATGATGATGATGATGATGATGATGATG 840
DB 968 GATTCACACGAGTGAACACCTTCTGATGATGATGATGATGATGATGATGATGATGATG 1027
QY 841 CGCAGCGCAGAGGTTGCGCGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
DB 1028 CGCAGCGCAGAGGTTGCGCGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1087
QY 901 TTGACGCGCCCAATCCACCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
DB 1088 TTGACGCGCCCAATCCACCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1147
QY 961 TTTATCGCGGACAGATTAATCTGCGCAATCTGCGCGGCGGCGGCGGCGGCGGCGGCGG 1020
DB 1148 TTTATCGCGGACAGATTAATCTGCGCAATCTGCGCGGCGGCGGCGGCGGCGGCGGCGG 1207
QY 1021 AGCTTCCCGGTCAGCGGAGTAACCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
DB 1208 AGCTTCCCGGTCAGCGGAGTAACCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1267
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Qy 1261 ATCGTGAATGAAGCAGCAGCATACCGCGTGCAGTTTGAGAT 1300
|||
Db 1448 ATCGTGAATGAAGCAGCAGCATACCGCGTGCAGTTTGTAAT 1487
|||

Search completed: December 18, 2003, 08:46:30
Job time : 5 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2003, 08:56:04 ; Search time 1 Seconds
(without alignments)

1.642 Million cell updates/sec

Title: us-09-866-379c-8

Perfect score: 2246

Sequence: 1 MXALLPFLSLIPLTPQSA.....CSLAGFTQIVNEARIPACSL 432

Scoring table:

	BLOSUM62
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1 seqs, 1901 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=soft -Q=us-09-866-379c-8 -DB=us-09-866-379c-7
-SUFFIX=ptc -OUT=align8_7 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO XLPXY
-NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : us-09-866-379c-7.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	2246	100.0	1901	us-09-866-379c-7

ALIGNMENTS

RESULT 1

us-09-866-379c-7

Alignment Scores:

Pred. No.:	0	Length:	1901
Scores:	2246.00	Matches:	432
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

us-09-866-379c-8 (1-432) x us-09-866-379c-7 (1-1901)

QY	1	MetLysAlaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla	20
DB	188	ATGAAGCGATCTTAATCCCACTTTTATCTCTCTGATTCGGTTAACCCCGCAATCTGCA	247

QY	21	PheAlaGlnSerGluProGluLeuLeuSerValValIleValSerArgHisGly	40
DB	248	TTGGCTCAGAGTGGAGCGGAGCTGAGCTGAAAGTGTGGTGAATGTTCAGTCTCATGGT	307
QY	41	ValArgAlaProThrLysAlaThrGlnMetClnAspValThrProAspAlaTrpPro	60
DB	308	GTGGCTGCTCCCAACCAAGGCCACGCAACTGATGACGAGATGTCACCCAGAGCGCATGGCCA	367
QY	61	ThrTrpProValLysLeuGlyTrpLeuThrProArgGlyGlyGluLeuIleAlaTrpLeu	80
DB	368	ACCTGGCCGGTAAACATGGGTGGCTGACACCGGCGGTGGTGGAGCTAATCGCTATCTC	427
QY	81	GlyHisTrpGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro	100
DB	428	GGACATTACCAAGCCAGCGGCTGCTGAGCCGACGGATTGCTGGCGMAAAGGGCTGCCCG	487
QY	101	GlnSerGlyGlnValAlaIleAlaAspValAspGluArgThrArgLysThrGlyGlu	120
DB	488	CAGTCTGGTCAAGTCCGATTAATGCTGATGTCGACGAGCGTACCCGTAAACAGCGCGAA	547
QY	121	AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr	140
DB	548	GCCTTCGCGCGCGGCTGGCACCTGCTGTCGATTAACCGTACATACCCAGCGCATAGC	607
QY	141	SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla	160
DB	608	TCCAGTCCCGATCCGTTATTAATCTCTAATAACTGGCGTTGTCAACTGATTAACGCG	667
QY	161	AsnValThrAspAlaIleLeuSerThrArgAlaGlySerIleAlaAspPheThrGlyHis	180
DB	668	AACGTGACTGACGCGATCTCAGCAGGCGAGGCTCAATGCTGACTTTTACCGGGCAT	727
QY	181	ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys	200
DB	728	CGGCAACGCGCGCTTCGCGAATCGTGAACGCGGTCTTAATTTCCCAATCAACTGTGCG	787
QY	201	LeuLysArgGluLeuGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr	220
DB	788	CTTAAACGTGAGAAACAGACGAGAAAGCTGTTCAATTAACGAGGCTTACCATCGGAATC	847
QY	221	LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr	240
DB	848	AAGGTGAGCGCGCAATGCTCTCAATACCGGTGCGTAAGCTTCGATCAATGCTGACG	907
QY	241	GluIlePheLeuLeuGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr	260
DB	908	GAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCCGGGTGGGGAAGGATCAC	967
QY	261	AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTrpLeuGln	280
DB	968	GATTCACACAGTGGAAACACTTGTAGTTTGCATAACGCGCAATTTTATTGCTACAA	1027
QY	281	ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla	300
DB	1028	CGCACGCCAGAGTTCGCCCGCGCGCCCGGATGATGATGATGATGATGATGATGATGAT	1087
QY	301	LeuThrProHisProGlnLysGlnAlaTrpGlyValThrLeuProThrSerValLeu	320
DB	1088	TTGACGCCCCCTCCACCGCAAAACAGGCGTATGATGATGATGATGATGATGATGATGAT	1147
QY	321	PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp	340
DB	1148	TTTATCGCGGACACGATACTAATCTGCGCAATCTCGGCGGCGCACTGAGAGCTCACTG	1207
QY	341	ThrLeuProGlyClnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp	360
DB	1208	ACGCTTCCCGGTGACGCGCGATTAACACGCGCGAGGTGGTGAACCTGTGTGTTGACCTG	1267
QY	361	ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln	380
DB	1268	CGTCGCTAAGCGATTAACAGCCAGTGGATTCAGTTTCGTTCTGCTTCCAGCTTACAG	1327

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QY 381 GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400
Db 1328 CAGATCGGTGATATAACGCCGCTGTCTTAAATACCCGCCGAGGTGAACAGCC 1387

QY 401 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420
Db 1388 CTGGCAGGATGTCAAGAGCGCAATGCGCAGGCGATGTTGTTGTCAGGTTTACGCAA 1447

QY 421 IleValAsnGluAlaArgIleProAlaCysSerLeu 432
Db 1448 ATCGTGAATGACGCGCATACCGCGTGCAGTTG 1483

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Search completed: December 18, 2003, 08:56:07
Job time : 3 secs

QY	381	GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValIysLeuThr	400
DB	1141	CAGATGGTGTATATAAAGCCGCTGTCTTAAATACGCGCGCCGAGAGGTGAACCTGACC	1200
QY	401	LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln	420
DB	1201	CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCTGTTGCCAGGTTTACGCRA	1260
QY	421	IleValAsnGluAlaArgIleProAlaCysSerLeu	432
DB	1261	ATCGTGATGAGACCGCATACCGCGCGTGCAGTTTG	1296

Search completed: December 18, 2003, 08:56:52
 Job time : 2 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 08:49:27 ; Search time 0.001 Seconds
(without alignments)
186.624 Million cell updates/sec

Title: us-09-866-379c-8

Perfect score: 2246

Sequence: 1 MKAILPFLSLIPLTPQSA.....CSLAGTQIVNEARIPACSL 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 432 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : us-09-866-379c-10.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2182	97.2	432	1	us-09-866-379c-10

ALIGNMENTS

RESULT 1
us-09-866-379c-10

Query Match 97.2%; Score 2182; DB 1; Length 432;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 424; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	1	MKAILPFLSLIPLTPQSA	PELKLESVIVSRHGVRA	PTKATQ	LMQDVT	PDAMP	60
DB	1	MKAILPFLSLIPLTPQSA	PELKLESVIVSRHGVRA	PTKATQ	LMQDVT	PDAMP	60
QY	61	TWPKLGLTPRGS	LIPLTPQSA	PELKLESVIVSRHGVRA	PTKATQ	LMQDVT	PDAMP
DB	61	TWPKLGLTPRGS	LIPLTPQSA	PELKLESVIVSRHGVRA	PTKATQ	LMQDVT	PDAMP
QY	121	AFRAGLAPCAITVHTQ	ADTSSPDPL	ENPLKTVG	COLDNANVT	DAILSRAGGS	TADEFTGH
DB	121	AFRAGLAPCAITVHTQ	ADTSSPDPL	ENPLKTVG	COLDNANVT	DAILSRAGGS	TADEFTGH
QY	181	ROTAFLRELRVNF	FPQSNICL	AREKQDE	SCSLTQAL	PSLKVSA	DNVSLTCAVSLASMLT
DB	181	ROTAFLRELRVNF	FPQSNICL	AREKQDE	SCSLTQAL	PSLKVSA	DNVSLTCAVSLASMLT
QY	241	EIFLLQQAQCP	EPGNGRIT	DSHOWNTLL	SLHNAQ	FPYLLQ	RTPEVARSRA
DB	241	EIFLLQQAQCP	EPGNGRIT	DSHOWNTLL	SLHNAQ	FPYLLQ	RTPEVARSRA

QY 301 LTPHPPOKQAYGVTLPTSVLFIAGHDYTNLANLGGALELNWTLPCQPDNTFPFGSELVFERW 360
DB 301 LTPHPPOKQAYGVTLPTSVLFIAGHDYTNLANLGGALELNWTLPCQPDNTFPFGSELVFERW 360
QY 361 RLSDNSOWIOVSLVFQTLQOVRDKTPLSLNTPPGVEVKLTLAGCEERNAQMCSLAGTQ 420
DB 361 RLSDNSOWIOVSLVFQTLQOVRDKTPLSLNTPPGVEVKLTLAGCEERNAQMCSLAGTQ 420
QY 421 IVNEARIPACSL 432
DB 421 IVNEARIPACSL 432

Search completed: December 18, 2003, 08:49:28
Job time : 1 secs